

0280
04/15

OIPE

#2

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/10/003,919

DATE: 12/12/2001
 TIME: 14:26:26

Input Set : A:\RTS-0256 Sequence Listing.txt
 Output Set: N:\CRF3\12112001\I003919.raw

ENTERED

6 <110> APPLICANT: C. Frank Bennett
 7 Susan M. Freier
 9 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF SHIP-1 EXPRESSION
 11 <130> FILE REFERENCE: RTS-0256
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/003,919
 C--> 13 <141> CURRENT FILING DATE: 2001-12-06
 13 <160> NUMBER OF SEQ ID NOS: 87
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 20
 18 <212> TYPE: DNA
 19 <213> ORGANISM: Artificial Sequence
 21 <220> FEATURE:
 23 <223> OTHER INFORMATION: Antisense Oligonucleotide
 25 <400> SEQUENCE: 1
 26 tccgtcatcg ctcctcaggg 20
 29 <210> SEQ ID NO: 2
 30 <211> LENGTH: 20
 31 <212> TYPE: DNA
 32 <213> ORGANISM: Artificial Sequence
 34 <220> FEATURE:
 36 <223> OTHER INFORMATION: Antisense Oligonucleotide
 38 <400> SEQUENCE: 2
 39 atgcattctg ccccaagga 20
 42 <210> SEQ ID NO: 3
 43 <211> LENGTH: 5273
 44 <212> TYPE: DNA
 45 <213> ORGANISM: Homo sapiens
 47 <220> FEATURE:
 49 <220> FEATURE:
 50 <221> NAME/KEY: CDS
 51 <222> LOCATION: (513)...(4079)
 53 <400> SEQUENCE: 3
 54 cttagggatcg gcatccccacg tgggtgtcag cacggccgca gaagaaccac ttctctggcc 60
 55 cacccatgcc tcgttaggcac tggttcttca gaagtggcca caactctcc gacgtctcca 120
 58 gagccgtca ttccaccccg ggggacttca gctgcactg gacacttcaa ttgtacgtg 180
 60 cgaccatgtt ccagaagaa gagggctggc aagaaagccg cggcagccgt ggcagggtgt 240
 62 atgggacgtt ggacggcccg ggcccccccc ttcctcttttctctctc tctcttgcct 300
 64 ggtttctgtta atgaggaagt ttcgcgcage tcagtttctt ttccctcaact gagegcctga 360
 66 aacaggaagt cagtcaatc agctgggtgc agcagccgag gccaccaaga ggcaacgggc 420
 68 ggcagggttc agtggggggg cttccgttcc cctcggttgt gtgtgggtcc tgggggtgcc 480
 70 tgccggccca gccgaggagg cccacgccccca cc atg gtc ccc tgc tgg aac cat 533
 71 Met Val Pro Cys Trp Asn His
 72 1 5
 74 ggc aac atc acc cgc tcc aag gcg gag gag ctg ctt tcc agg aca ggc 581
 75 Gly Asn Ile Thr Arg Ser Lys Ala Glu Glu Leu Leu Ser Arg Thr Gly
 76 10 15 20
 78 aag gac ggg agc ttc ctc gtg cgt gcc agc gag tcc atc tcc cgg gca 629

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79	Lys	Asp	Gly	Ser	Phe	Leu	Val	Arg	Ala	Ser	Glu	Ser	Ile	Ser	Arg	Ala
80	25					30					35					
82	tac	gcg	ctc	tgc	gtg	ctg	tat	cgg	aat	tgc	gtt	tac	act	tac	aga	att
83	Tyr	Ala	Leu	Cys	Val	Leu	Tyr	Arg	Asn	Cys	Val	Tyr	Thr	Tyr	Arg	Ile
84	40					45					50					55
86	ctg	ccc	aat	gaa	gat	gat	aaa	ttc	act	gtt	cag	gca	tcc	gaa	ggc	gtc
87	Leu	Pro	Asn	Glu	Asp	Asp	Lys	Phe	Thr	Val	Gln	Ala	Ser	Glu	Gly	Val
88						60				65					70	
90	tcc	atg	agg	ttc	acc	aag	ctg	gac	cag	ctc	atc	gag	ttt	tac	aag	
91	Ser	Met	Arg	Phe	Phe	Thr	Lys	Leu	Asp	Gln	Leu	Ile	Glu	Phe	Tyr	Lys
92						75				80				85		
94	aag	gaa	aac	atg	ggg	ctg	gtg	acc	cat	ctg	caa	tac	cct	gtg	ccg	ctg
95	Lys	Glu	Asn	Met	Gly	Leu	Val	Thr	His	Leu	Gln	Tyr	Pro	Val	Pro	Leu
96						90				95				100		
98	gag	gaa	gag	gac	aca	ggc	gac	gac	cct	gag	gag	gac	aca	gaa	agt	gtc
99	Glu	Glu	Asp	Thr	Gly	Asp	Asp	Pro	Glu	Glu	Glu	Asp	Thr	Glu	Ser	Val
100						105				110				115		
102	gtg	tct	cca	ccc	gag	ctg	ccc	cca	aga	aac	att	ccg	ctg	act	gcc	agc
103	Val	Ser	Pro	Pro	Glu	Leu	Pro	Pro	Arg	Asn	Ile	Pro	Leu	Thr	Ala	Ser
104	120					125					130				135	
106	tcc	tgt	gag	gcc	aag	gag	gtt	cct	ttt	tca	aac	gag	aat	ccc	cga	gct
107	Ser	Cys	Glu	Ala	Lys	Glu	Val	Pro	Phe	Ser	Asn	Glu	Asn	Pro	Arg	Ala
108						140				145				150		
110	acc	gag	acc	agc	cg	ccg	agc	ctc	tcc	gag	aca	ttt	ccg	cga	ctg	
111	Thr	Glu	Thr	Ser	Arg	Pro	Ser	Leu	Ser	Glu	Thr	Leu	Phe	Gln	Arg	Leu
112						155				160				165		
114	caa	agg	atg	gac	acc	agt	ggg	ctt	cca	gaa	gag	cat	ctt	aag	gcc	atc
115	Gln	Ser	Met	Asp	Thr	Ser	Gly	Leu	Pro	Glu	Glu	His	Leu	Lys	Ala	Ile
116						170				175				180		
118	caa	gat	tat	tta	agc	act	cag	ctc	gcc	cag	gac	tct	gaa	ttt	gtg	aag
119	Gln	Asp	Tyr	Leu	Ser	Thr	Gln	Leu	Ala	Gln	Asp	Ser	Glu	Phe	Val	Lys
120						185				190				195		
122	aca	ggg	tcc	agc	agt	ctt	cct	cac	ctg	aag	aaa	ctg	acc	aca	ctg	ctc
123	Thr	Gly	Ser	Ser	Leu	Pro	His	Leu	Lys	Lys	Leu	Thr	Thr	Leu	Leu	
124	200					205					210				215	
126	tgc	aag	gag	ctc	tat	gga	gaa	gtc	atc	ccg	acc	ctc	cca	tcc	ctg	gag
127	Cys	Lys	Glu	Leu	Tyr	Gly	Glu	Val	Ile	Arg	Thr	Leu	Pro	Ser	Leu	Glu
128						220				225				230		
130	tct	ctg	cag	agg	tta	ttt	gac	cag	cag	ctc	tcc	ccg	ggc	ctc	cgt	cca
131	Ser	Leu	Gln	Arg	Leu	Phe	Asp	Gln	Gln	Leu	Ser	Pro	Gly	Leu	Arg	Pro
132						235				240				245		
134	cgt	cct	cag	gg	ttt	ggt	gag	gcc	aat	ccc	atc	aac	atg	gtg	tcc	aag
135	Arg	Pro	Gln	Val	Pro	Gly	Glu	Ala	Asn	Pro	Ile	Asn	Met	Val	Ser	Lys
136						250				255				260		
138	ctc	agg	caa	ctg	aca	agc	ctg	tca	tcc	att	gaa	gac	aag	gtc	aag	
139	Leu	Ser	Gln	Leu	Thr	Ser	Leu	Leu	Ser	Ser	Ile	Glu	Asp	Lys	Val	Lys
140						265				270				275		
142	gcc	ttt	ctg	cac	gag	gg	cct	gag	tct	ccg	cac	ccg	ccc	tcc	ctt	atc
143	Ala	Leu	Leu	His	Glu	Gly	Pro	Glu	Ser	Pro	His	Arg	Pro	Ser	Leu	Ile

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144	280	285	290	295	
146	cct cca gtc acc ttt gag	gtg aag gca gag	tct ctg ggg att	cct cag	1445
147	Pro Pro Val Thr Phe Glu	Val Lys Ala Glu Ser	Leu Gly Ile Pro	Gln	
148	300	305	310		
150	aaa atg cag ctc aaa gtc gac	gtt gag tct ggg aaa	ctg atc att aag		1493
151	Lys Met Gln Leu Lys Val Asp	Val Glu Ser Gly Lys	Leu Ile Ile Lys		
152	315	320	325		
154	aag tcc aag gat ggt tct gag	gac aag ttc tac	agc cac aag aaa	atc	1541
155	Lys Ser Lys Asp Gly Ser	Glu Asp Lys Phe Tyr	Ser His Lys Lys Ile		
156	330	335	340		
158	ctg cag ctc att aag tca	cag aaa ttt ctg aat aag	ttg gtg atc ttg		1589
159	Leu Gln Leu Ile Lys Ser Gln	Lys Phe Leu Asn Lys	Leu Val Ile Leu		
160	345	350	355		
162	gtg gaa aca gag aag gag	aag atc ctg cgg aag	gaa tat gtt ttt	gct	1637
163	Val Glu Thr Glu Lys Glu	Ile Leu Arg Lys Clu	Tyr Val Phe Ala		
164	360	365	370	375	
166	gac tcc aaa aag aga gaa	ggc ttc tgc cag	ctc ctg cag cag	atg aag	1685
167	Asp Ser Lys Lys Arg Glu	Gly Phe Cys Gln	Leu Leu Gln Gln	Met Lys	
168	380	385	390		
170	aac aag cac tca gag cag	ccg gag ccc gac	atg atc acc atc	ttc atc	1733
171	Asn Lys His Ser Glu Gln	Pro Glu Pro Asp	Met Ile Thr Ile	Phe Ile	
172	395	400	405		
174	ggc acc tgg aac atg ggt	aac gcc ccc cct	ccc aag aag atc acg	tcc	1781
175	Gly Thr Trp Asn Met Gly	Asn Ala Pro Pro	Lys Lys Ile Thr	Ser	
176	410	415	420		
178	tgg ttt ctc tcc aag ggg	cag gga aag acg	cgg gac gac	tct gcg gac	1829
179	Trp Phe Leu Ser Lys Gly	Gln Gly Lys Thr	Arg Asp Asp Ser Ala Asp		
180	425	430	435		
182	tac atc ccc cat gac	att tac gtg atc	ggc acc caa gag	gac ccc ctg	1877
183	Tyr Ile Pro His Asp Ile	Tyr Val Ile Gly	Thr Gln Glu Asp	Pro Leu	
184	440	445	450	455	
186	agt gag aag gag tgg	ctg gag atc ctc	aaa cac tcc ctg	caa gaa atc	1925
187	Ser Glu Lys Glu Trp	Leu Glu Ile	Leu Lys His Ser	Leu Gln Glu Ile	
188	460	465	470		
190	acc agt gtg act ttt	aaa aca gtc gcc	atc cac acg	ctc tgg aac atc	1973
191	Thr Ser Val Thr Phe Lys	Thr Val Ala Ile	His Thr Leu Trp	Asn Ile	
192	475	480	485		
194	cgc atc gtg gtg ctg	gcc aag cct gag	cac gag aac	cgg atc agc cac	2021
195	Arg Ile Val Val Leu Ala	Lys Pro Glu His	Glu Asn Arg Ile	Ser His	
196	490	495	500		
198	atc tgt act gac aac	gtg aag aca ggc	att gca aac aca	ctg ggg aac	2069
199	Ile Cys Thr Asp Asn Val	Lys Thr Gly Ile	Ala Asn Thr	Leu Gly Asn	
200	505	510	515		
202	aag gga gcc gtg	ggg gtg tcg	ttc atg ttc	aat gga acc tcc tta	2117
203	Lys Gly Ala Val Gly	Val Ser Phe Met	Phe Asn Gly	Thr Ser Leu Gly	
204	520	525	530	535	
206	tcc gtc aac agc cac	ttg act tca	gga agt gaa aag	aaa ctc agg cga	2165
207	Phe Val Asn Ser His	Leu Thr Ser Gly	Ser Glu Lys	Lys Leu Arg Arg	
208	540	545	550		

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210 aac caa aac tat atg aac att ctc cgg ttc ctg gcc ctg ggc gac aag	2213
211 Asn Gln Asn Tyr Met Asn Ile Leu Arg Phe Leu Ala Leu Gly Asp Lys	
212 555 560 565	
214 aag ctg agt ccc ttt aac atc act cac cgc ttc acg cac ctc ttc tgg	2261
215 Lys Leu Ser Pro Phe Asn Ile Thr His Arg Phe Thr His Leu Phe Trp	
216 570 575 580	
218 ttt ggg gat ctt aac tac cgt gtg gat ctg cct acc tgg gag gca gaa	2309
219 Phe Gly Asp Leu Asn Tyr Arg Val Asp Leu Pro Thr Trp Glu Ala Glu	
220 585 590 595	
222 acc atc atc caa aaa atc aag cag cag tac gca gac ctc ctg tcc	2357
223 Thr Ile Ile Gln Lys Ile Lys Gln Gln Gln Tyr Ala Asp Leu Leu Ser	
224 600 605 610 615	
226 cac gac cag ctg ctc aca gag agg gag cag aag gtc ttc cta cac	2405
227 His Asp Gln Leu Leu Thr Glu Arg Arg Glu Gln Lys Val Phe Leu His	
228 620 625 630	
230 ttc gag gag gaa gaa atc acg ttt gcc cca acc tac cgt ttt gag aga	2453
231 Phe Glu Glu Glu Ile Thr Phe Ala Pro Thr Tyr Arg Phe Glu Arg	
232 635 640 645	
234 ctg act cgg gac aaa tac gcc tac acc aag cag aaa gcg aca ggg atg	2501
235 Leu Thr Arg Asp Lys Tyr Ala Tyr Thr Lys Gln Lys Ala Thr Gly Met	
236 650 655 660	
238 aag tac aac ttg cct tcc ttg tgt gac cga gtc ctc tgg aag tct tat	2549
239 Lys Tyr Asn Leu Pro Ser Trp Cys Asp Arg Val Leu Trp Lys Ser Tyr	
240 665 670 675	
242 ccc ctg gtg cac gtg gtg tgt cag tct tat ggc agt acc agc gac atc	2597
243 Pro Leu Val His Val Val Cys Gln Ser Tyr Gly Ser Thr Ser Asp Ile	
244 680 685 690 695	
246 atg acg agt gac cac agc cct gtc ttt gcc aca ttt gag gca gga gtc	2645
247 Met Thr Ser Asp His Ser Pro Val Phe Ala Thr Phe Glu Ala Gly Val	
248 700 705 710	
250 act tcc cag ttt gtc tcc aag aac ggt ccc ggg act gtt gac agc caa	2693
251 Thr Ser Gln Phe Val Ser Lys Asn Gly Pro Gly Thr Val Asp Ser Gln	
252 715 720 725	
254 gga cag att gag ttt ctc agg tgc tat gcc aca ttg aag acc aag tcc	2741
255 Gly Gln Ile Glu Phe Leu Arg Cys Tyr Ala Thr Leu Lys Thr Lys Ser	
256 730 735 740	
258 cag acc aaa ttc tac ctg gag ttc cac tcg agc tgc ttg gag agt ttt	2789
259 Gln Thr Lys Phe Tyr Leu Glu Phe His Ser Ser Cys Leu Glu Ser Phe	
260 745 750 755	
262 gtc aag agt cag gaa gga gaa aat gaa gaa gga agt gag ggg gag ctg	2837
263 Val Lys Ser Gln Glu Gly Glu Asn Glu Glu Gly Ser Glu Gly Glu Leu	
264 760 765 770 775	
266 gtg gtg aag ttt ggt gag act ctt cca aag ctg aag ccc att atc tct	2885
267 Val Val Lys Phe Gly Glu Thr Leu Pro Lys Leu Lys Pro Ile Ile Ser	
268 780 785 790	
270 gac cct gag tac ctg cta gac cag cac atc ctc atc agc atc aag tcc	2933
271 Asp Pro Glu Tyr Leu Leu Asp Gln His Ile Leu Ile Ser Ile Lys Ser	
272 795 800 805	
274 tct gac agc gac gaa tcc tat ggc gag ggc tgc att gcc ctt cgg tta	2981

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275	Ser	Asp	Ser	Asp	Glu	Ser	Tyr	Gly	Glu	Gly	Cys	Ile	Ala	Leu	Arg	Leu
276		810			815							820				
278	gag	gcc	aca	gaa	acg	cag	ctg	ccc	atc	tac	acg	cct	ctc	acc	cac	cat
279	Glu	Ala	Thr	Glu	Thr	Gln	Leu	Pro	Ile	Tyr	Thr	Pro	Leu	Thr	His	His
280		825					830					835				
282	ggg	gag	ttg	aca	ggc	cac	ttc	cag	ggg	gag	atc	aag	ctg	cag	acc	tct
283	Gly	Glu	Leu	Thr	Gly	His	Phe	Gln	Gly	Glu	Ile	Lys	Leu	Gln	Thr	Ser
284		840			845						850			855		
286	cag	ggc	aag	acg	agg	gag	aag	ctc	tat	gac	ttt	gtg	aag	acg	gag	cgt
287	Gln	Gly	Lys	Thr	Arg	Glu	Lys	Leu	Tyr	Asp	Phe	Val	Lys	Thr	Glu	Arg
288			860				865				870					
290	gat	gaa	tcc	agt	ggg	cca	aag	acc	ctg	aag	agc	ctc	acc	agc	cac	gac
291	Asp	Glu	Ser	Ser	Gly	Pro	Lys	Thr	Leu	Lys	Ser	Leu	Thr	Ser	His	Asp
292			875					880			885					
294	ccc	atg	aag	cag	tgg	gaa	gtc	act	agc	agg	gcc	cct	ccg	tgc	agt	ggc
295	Pro	Met	Lys	Gln	Trp	Glu	Val	Thr	Ser	Arg	Ala	Pro	Pro	Cys	Ser	Gly
296		890					895				900					
298	tcc	agc	atc	act	gaa	atc	atc	aac	ccc	aac	tac	atg	gga	gtg	ggg	ccc
299	Ser	Ser	Ile	Thr	Glu	Ile	Ile	Asn	Pro	Asn	Tyr	Met	Gly	Val	Gly	Pro
300		905					910				915					
302	ttt	ggg	cca	cca	atg	ccc	ctg	cac	gtg	aag	cat	ggc	cct	ccg	tgc	atg
303	Phe	Gly	Pro	Pro	Met	Pro	Leu	His	Val	Lys	Gln	Thr	Leu	Ser	Pro	Asp
304		920				925				930			935			
306	cag	cag	ccc	aca	gcc	tgg	agc	tac	gac	cag	ccg	ccc	aag	gac	tcc	ccg
307	Gln	Gln	Pro	Thr	Ala	Trp	Ser	Tyr	Asp	Gln	Pro	Pro	Lys	Asp	Ser	Pro
308			940				945				950					
310	ctg	ggg	ccc	tgc	agg	gga	gaa	agt	cct	ccg	aca	cct	ccc	ggc	cag	ccg
311	Leu	Gly	Pro	Cys	Arg	Gly	Glu	Ser	Pro	Pro	Thr	Pro	Pro	Gly	Gln	Pro
312			955				960				965					
314	ccc	ata	tca	ccc	aag	aag	ttt	tta	ccc	tca	aca	gca	aac	cg	gg	ctc
315	Pro	Ile	Ser	Pro	Lys	Lys	Phe	Leu	Pro	Ser	Thr	Ala	Asn	Arg	Gly	Leu
316		970					975				980					
318	cct	ccc	agg	aca	cag	gag	tca	agg	ccc	agt	gac	ctg	ggg	aag	aac	gca
319	Pro	Pro	Arg	Thr	Gln	Glu	Ser	Arg	Pro	Ser	Asp	Leu	Gly	Lys	Asn	Ala
320		985					990				995					
322	ggg	gac	acg	ctg	cct	cag	gag	gac	ctg	ccg	ctg	acg	aag	ccc	gag	atg
323	Gly	Asp	Thr	Leu	Pro	Gln	Glu	Asp	Leu	Pro	Leu	Thr	Lys	Pro	Glu	Met
324		1000			1005				1010			1015				
326	ttt	gag	aac	ccc	ctg	tat	ggg	tcc	ctg	agt	tcc	ttc	cct	aag	cct	gct
327	Phe	Glu	Asn	Pro	Leu	Tyr	Gly	Ser	Leu	Ser	Ser	Phe	Pro	Lys	Pro	Ala
328			1020				1025				1030					
330	ccc	agg	aag	gac	cag	gaa	tcc	ccc	aaa	atg	ccg	ccg	aag	gaa	ccc	ccg
331	Pro	Arg	Lys	Asp	Gln	Glu	Ser	Pro	Lys	Met	Pro	Arg	Lys	Glu	Pro	Pro
332			1035				1040				1045					
334	ccc	tgc	ccg	gaa	ccc	ggc	atc	ttg	tgc	ccc	acg	atc	gtg	ctc	acc	aaa
335	Pro	Cys	Pro	Glu	Pro	Gly	Ile	Leu	Ser	Pro	Ser	Ile	Val	Leu	Thr	Lys
336		1050			1055			1060				1060				
338	gcc	cag	gag	gct	gat	cgc	ggc	gag	ggg	ccc	ggc	aag	cag	gtg	ccc	ggc
339	Ala	Gln	Glu	Ala	Asp	Arg	Gly	Glu	Gly	Pro	Gly	Lys	Gln	Val	Pro	Ala

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L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date